

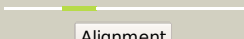

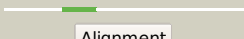
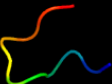


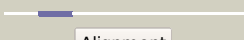
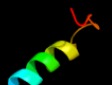



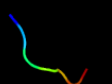

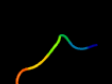

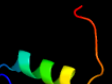




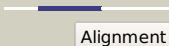
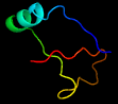
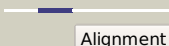
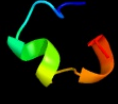
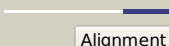

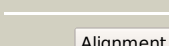
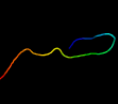
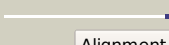

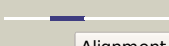


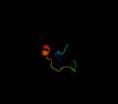




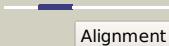
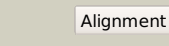
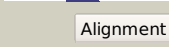
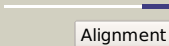
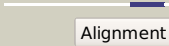
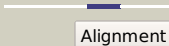




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1374c_(-)_1547078_1547536
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	e08e8c9e6ac93ee4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nv4A_</a>	 Alignment		65.1	90	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0066 protein af_0241; <b>PDBTitle:</b> crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
2	<a href="#">d1xqba_</a>	 Alignment		62.9	60	<b>Fold:</b> YaeB-like <b>Superfamily:</b> YaeB-like <b>Family:</b> YaeB-like
3	<a href="#">c3okxA_</a>	 Alignment		58.5	90	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yaeb-like protein rpa0152; <b>PDBTitle:</b> crystal structure of yaeb-like protein from rhodospseudomonas palustris
4	<a href="#">c5sydA_</a>	 Alignment		16.2	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> azurin, chimeric construct; <b>PDBTitle:</b> circularly permuted azurin (cpaz) based on p. aeruginosa azurin2 sequence
5	<a href="#">c2zihC_</a>	 Alignment		14.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74
6	<a href="#">c2mmbA_</a>	 Alignment		14.4	67	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein yp_001712342.1 from acinetobacter2 baumannii
7	<a href="#">c2btwA_</a>	 Alignment		13.5	71	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alr0975 protein; <b>PDBTitle:</b> crystal structure of alr0975
8	<a href="#">d2bu3a1</a>	 Alignment		13.5	71	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Phytochelatin synthase
9	<a href="#">c2ziiA_</a>	 Alignment		12.1	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 74; <b>PDBTitle:</b> crystal structure of yeast vps74-n-term truncation variant
10	<a href="#">c5xonW_</a>	 Alignment		10.6	30	<b>PDB header:</b> transcription/rna <b>Chain:</b> W: <b>PDB Molecule:</b> protein that forms a complex with spt4p; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with spt4/5 and tfiis
11	<a href="#">c6dgaA_</a>	 Alignment		10.0	67	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rpfr; <b>PDBTitle:</b> cronobacter turicensis rpfr quorum-sensing receptor rpfr interaction2 domain

12	<a href="#">c2qahA</a>	 Alignment		9.7	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-pyrone-4,6-dicarboxylic acid hydrolase; <b>PDBTitle:</b> crystal structure of the 2-pyrone-4,6-dicarboxylic acid hydrolase from <i>Sphingomonas paucimobilis</i>
13	<a href="#">c2n07X</a>	 Alignment		9.5	41	<b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> alpha-conotoxin vc1a; <b>PDBTitle:</b> design of a highly stable disulfide-deleted mutant of analgesic cyclic2 alpha-conotoxin vc1.1
14	<a href="#">c2hd0D</a>	 Alignment		9.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protease ns2-3 (p23); <b>PDBTitle:</b> structure of the catalytic domain of hepatitis c virus ns2
15	<a href="#">d2b5id2</a>	 Alignment		8.6	44	<b>Fold:</b> Complement control module/SCR domain <b>Superfamily:</b> Complement control module/SCR domain <b>Family:</b> Complement control module/SCR domain
16	<a href="#">c4u6uC</a>	 Alignment		8.4	23	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> cog7; <b>PDBTitle:</b> crystal structure of the cog5-cog7 complex from <i>Kluyveromyces lactis</i>
17	<a href="#">d1ovle</a>	 Alignment		8.3	67	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
18	<a href="#">c6ir9W</a>	 Alignment		8.3	30	<b>PDB header:</b> transcription/rna/dna <b>Chain:</b> W: <b>PDB Molecule:</b> spt5; <b>PDBTitle:</b> rna polymerase ii elongation complex bound with elf1 and spt4/5,2 stalled at shl(-1) of the nucleosome
19	<a href="#">c6buzN</a>	 Alignment		8.2	50	<b>PDB header:</b> structural protein/dna <b>Chain:</b> N: <b>PDB Molecule:</b> maltose-binding periplasmic protein, centromere protein n <b>PDBTitle:</b> cryo-em structure of cenp-a nucleosome in complex with kinetochore2 protein cenp-n
20	<a href="#">c4ph8B</a>	 Alignment		7.3	100	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> aggregative adherence fimbrial subunit agga; <b>PDBTitle:</b> crystal structure of agga, the major subunit of aggregative adherence2 fimbriae type i (aaf/i) from the <i>Escherichia coli</i> o4h104
21	<a href="#">c6cqxA</a>	 Alignment	not modelled	6.8	47	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-conotoxin vc1a; <b>PDBTitle:</b> backbone cyclised conotoxin vc1.1 mutant - d11a, e14a
22	<a href="#">c5l6nL</a>	 Alignment	not modelled	6.7	75	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> thrombin inhibitor madanin 1; <b>PDBTitle:</b> disulfated madanin-thrombin complex
23	<a href="#">d1tcaa</a>	 Alignment	not modelled	6.3	36	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
24	<a href="#">d2i15a1</a>	 Alignment	not modelled	6.2	32	<b>Fold:</b> MG296-like <b>Superfamily:</b> MG296-like <b>Family:</b> MG296-like
25	<a href="#">c6re80</a>	 Alignment	not modelled	5.7	56	<b>PDB header:</b> proton transport <b>Chain:</b> O: <b>PDB Molecule:</b> asa-10: polytomella f-atp synthase associated subunit 10; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map
26	<a href="#">c3rj1P</a>	 Alignment	not modelled	5.6	14	<b>PDB header:</b> transcription <b>Chain:</b> P: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 17; <b>PDBTitle:</b> architecture of the mediator head module
27	<a href="#">c3ez0D</a>	 Alignment	not modelled	5.4	54	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein with ferritin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with ferritin-like2 fold (yp_832262.1) from <i>Arthrobacter</i> sp. fb24 at 2.33 a resolution
28	<a href="#">d1b8xa1</a>	 Alignment	not modelled	5.3	25	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like

